

Genomic regions mapping of phenological, morphological and physiological traits of barley under salinity stress conditions

Abstract

Salinity stress is genetically and physiologically complex trait, controlled by quantitative trait loci (QTL). So, the identification of genes whose expression enables plants to tolerate salinity stress is essential for breeding programs. In order to genomic regions mapping associated with salinity tolerance in barley and to determine the portion of each QTL in the phenotypic variation of the related trait, 72 doubled-haploid lines, their two parents Steptoe and Morex, in year 2011-2012 completely randomized block design with two replications at the Research Farm of Agriculture College of Zabol University were conducted under normal and salinity stress conditions. The studied traits were phenologic traits, morphologic and physiologic traits including chlorophyll contents, chlorophyll fluorescence (Fo, Fm, Fv/Fm), leaf prolin content, relative water content (RWC). After measuring traits, statistical analysis such as ANOVA, correlation between traits, cluster analysis, stepwise regression, principle component analysis and factors analysis using SAS software was performed. Combined analysis of variance results showed significant difference between the lines for the whole of the studied traits. The maximum correlation was observed between heading to day with flowering to day ($r = 0.994^{**}$). In stepwise regression of traits grain number per spike and grain filling of period were first traits that entered to model and explained 90% of total variation in normal conditions and inter-node length, flag leaf with, plant height were first traits that entered the model in stress condition respectively and explained 43% of total variation. In PCA analysis, the first three principle components explained near 50% of the total variability in normal condition and first four principle components explained more of 50% of the total variability in stress condition.

Factors analysis extracted several invisible factor, when accounted for 80% of the variation and with to take into consideration characters pattern respectively are named as phenologic factor, plant article structural and yield factor, physiologic factor, product potential.

QTL analysis was carried out using genetic linkage map derived from 327 molecular marker of RFLP and QTL cartographer software with composite interval mapping method. In general we found 206 QTLs for studied traits, 62 QTLs for normal condition, 68 for salinity stress and 76 QTLs for mean of two conditions. Phenotypic variance that were explained by these QTLs, changed from 4.59 to 53.47. The highest and the lowest phenotypic variances were related to spike length and flowering to day in stress condition respectively. LOD was ranged in 2.51 to 13.99. The highest and the lowest LOD were attained for the QTLs of flowering to day (*qFTD2.2m*) in mean two conditions and to day (*qKTD3n*) in normal conditions.

Key word : QTL, salinity stress, barley, doubled-haploid lines



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